

PCT09

RAW SEQUENCE LISTING

DATE: 11/14/2001

PATENT APPLICATION: US/09/763,011A

TIME: 13:52:05

Input Set : A:\JAB-1415.txt

Output Set: N:\CRF3\11142001\I763011A.raw

5 <110> APPLICANT: Contreras, Roland
6 Nelissen, Bart
7 DeBacker, Marianne
8 Luyten, Walter
9 Viaene, Jasmine
10 Logghe, Marc George
13 <120> TITLE OF INVENTION: Drug Targets In Candida Albicans
16 <130> FILE REFERENCE: 50899/002
C--> 19 <140> CURRENT APPLICATION NUMBER: US/09/763,011A
C--> 21 <141> CURRENT FILING DATE: 2001-02-14
24 <150> PRIOR APPLICATION NUMBER: 98310694.9
26 <151> PRIOR FILING DATE: 1998-12-23
29 <150> PRIOR APPLICATION NUMBER: 9817796.7
31 <151> PRIOR FILING DATE: 1998-08-14
34 <160> NUMBER OF SEQ ID NOS: 114
38 <170> SOFTWARE: PatentIn Ver. 2.0
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44 <211> LENGTH: 1851
46 <212> TYPE: DNA
48 <213> ORGANISM: Candida albicans
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58 gataaaccat tgaaggaata tattggtatt agtattttgt gtttccttat tgcctttggt 180
60 ggtttcgttt ttggttttga tactggtacc atttctggtt tcattaacat gactgacttt 240
62 ttagaaagat ttggtggtac taaagctgac ggtactcttt acttttccaa cgttagaact 300
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66 gtcgggtgata tgtacggtga aagagttggt atcatgactg ctatgatcat ttatatgttt 420
68 ggtattattg ttcaaattgc ttctcaacat gcttggtatc aaatcatgat tggtagaatt 480
70 atcactgggc ttgctgttgg tatgttatca gttttgtgtc cattatttat ctcagagggt 540
72 tctcccaaac atttaagagg tacattagtt tattgtttcc aattgatgat taccttggtt 600
74 atttttcttg gttactgtac cagttacggt actaagaaat attctgactc cagacaatgg 660
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84 actggttaac caagaatcct tgaaagagtt attgttgagg gtatgttgca atcattgcaa 960
86 caattgactg gtgataacta tttcttctac tacagtacca ccattttcaa gtctgtcgggt 1020
88 ttaaattgatt ccttcgaaac atctattatc cttggtgtca tcaactttgc ttccactttt 1080
90 gttggtattt atgccattga aagattgggt agaagacttt gtttattaac tggttccggt 1140
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104 actaaagggt ttactttaga ggaaattgat gaattatact ctaccaaggt tgttccatgg 1560

Does Not Comply
Corrected Diskette Needed

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106 aaatcagccg gttgggttcc accttctgac gaagaaatgg ttcgtgcaaa aggctatact 1620
108 ggtgatatcc acgcagatga agagcaagtt taatcaactc tttgtcaatt aatgctgtac 1680
110 ttgttttcat tttatttgct ggcattttaa gaatacccat agttcagaaa ataaaattga 1740
112 aaaattttaa aaaaaacgca atatcattca tttttttgt ttttttgaca ataattattaa 1800
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142 ggttgatctc attgactaaa actaccctag ggataaatgc tgaaccgtgg ttaccaactg 420
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146 caactgttac attgctggta ctacattaag aataaatgct gcactacaaa gtaccacctg 540
148 ttgtgttaat aaatgctgca cctgctagta caactgttgc tggcatgat agttactaca 600
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158 <212> TYPE: DNA

160 <213> ORGANISM: Candida albicans

164 <400> SEQUENCE: 3

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170 acttcaaata acacaatatc aatacttaca aaccttttc aaatactaaa ggatttgcta 180
172 ccatatagca aaacttctaa accgcaaatc aaggaatcca gaccgttgat taaagttctg 240
174 agagatggag tgccaataaa tttccacagg gtcocggcta taataatgaa atcgaacaaa 300
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178 actgaatttg caactaccac tgtttccct acacaagaat ttcaagcact acagataaac 420
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182 attaccattg aagacacacc caaaacacta gaaccagaag aatcgtcaga tgctttgcag 540
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188 attgttccaa tttatactac acatatcgtc acttcggcga ttccatcgta tgtacaaaa 720
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212 aaatttgatg tgtttgattg gatatttgaa agtgggtacta ccaatgagaa agtacatgga 1440
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224 <213> ORGANISM: Candida albicans
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232 1 5 10 15
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238 20 25 30
242 Ile Ser Ile Leu Thr Asn His Phe Gln Ile Leu Lys Asp Leu Leu Pro
244 35 40 45
248 Tyr Ser Lys Thr Ser Lys Pro Gln Ile Lys Glu Ser Arg Pro Leu Ile
250 50 55 60
254 Lys Val Ser Arg Asp Gly Val Pro Ile Asn Phe His Arg Ala Pro Ala
256 65 70 75 80
260 Ile Ile Met Lys Ser Asn Lys Thr Asp Asp Leu Val Arg Asn Ser Asn
262 85 90 95
266 Lys Thr Met Val Leu Thr Glu Ile Lys Thr Ile Thr Glu Phe Ala Thr
268 100 105 110
272 Thr Thr Val Ser Pro Thr Gln Glu Phe Gln Ala Leu Gln Ile Asn Leu
274 115 120 125
278 Asn Thr Leu Ser Ile Glu Thr Ser Thr Pro Thr Phe Gln Ser His Asp
280 130 135 140
284 Phe Pro Pro Ile Thr Ile Glu Asp Thr Pro Lys Thr Leu Glu Pro Glu
286 145 150 155 160
290 Glu Ser Ser Asp Ala Leu Gln Arg Asp Ala Phe Asp Gln Ile Lys Lys
292 165 170 175
296 Leu Glu Lys Leu Val Leu Asp Leu Arg Leu Glu Met Lys Glu Gln Gln
298 180 185 190
302 Lys Ser Phe Asn Asp Gln Leu Val Asp Ile Tyr Thr Ala Arg Ser Ile
304 195 200 205
308 Val Pro Ile Tyr Thr Thr His Ile Val Thr Ser Ala Ile Pro Ser Tyr
310 210 215 220
314 Val Pro Lys Glu Glu Val Met Val Ser His Asp Thr Ala Pro Ile Val
316 225 230 235 240
320 Ser Arg Pro Arg Thr Asp Ile Pro Val Ser Gln Arg Ile Asp Thr Ile
322 245 250 255
326 Ser Lys His Lys Met Asn Gly Lys Asn Ile Leu Asn Asn Asn Pro Pro
328 260 265 270
332 Pro Asn Ser Val Leu Ile Val Pro Gln Phe Gln Phe His Glu Arg Met
334 275 280 285
338 Ala Thr Lys Thr Glu Val Ala Tyr Met Lys Pro Lys Ile Val Trp Thr
340 290 295 300
344 Asn Phe Pro Thr Thr Thr Ala Thr Ser Met Phe Asp Asn Phe Ile Leu
346 305 310 315 320
350 Lys Asn Leu Val Asp Glu Thr Asp Ser Glu Ile Asp Ser Gly Glu Thr
352 325 330 335

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358           340           345           350
362 Lys Glu Asp Asp Ser Asp Glu Ile Thr Ala Gln Ile Leu Leu Ser Asn
364           355           360           365
368 Ser Glu Leu Gly Thr Lys Thr Pro Asn Phe Glu Asp Pro Phe Glu Gln
370           370           375           380
374 Ile Asn Ile Glu Asp Asn Lys Val Ile Ser Val Asn Thr Pro Lys Thr
376 385           390           395           400
380 Lys Lys Pro Thr Thr Thr Val Phe Gly Thr Ser Thr Ser Ala Leu Ser
382           405           410           415
386 Thr Phe Glu Ser Thr Ile Phe Glu Ile Pro Lys Phe Phe Tyr Gly Ser
388           420           425           430
392 Arg Arg Lys Gln Ser Ser Ser Phe Lys Asn Lys Asn Ser Thr Ile Lys
394           435           440           445
398 Phe Asp Val Phe Asp Trp Ile Phe Glu Ser Gly Thr Thr Asn Glu Lys
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434 cgagaagatc atgaaaaatt taaagagatc aatatagcat atgaaacaat tagagattat 180
436 tatcaagaga atgggcaaaa gaacagtcaa ccgatcccta acacaaacac agagcataat 240
438 tcccatcaaa aaccacatta taacactggc ctttattcca catatcgttt tacgacctca 300
440 tctaccacga ctgataatac caatcacact ggacattcaa gttctcgggt tactttattat 360
442 aatttccacc aaaaagcgca agagaataac cgcaaacaag atgaagaaag ggcagcccaa 420
444 cgtgaacgat taaaaaagga gctcttccag aggcaacaag cggaagaagc acaacgaaag 480
446 aaggaatttg acaaaaaggc cgaattcatc aaagcatcat tacttgaaat gcgccgaaga 540
448 gaaatagaga ggcggaacaa gcaaaaggaa agggaacaaa gacaaaagga gcacgaagca 600
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452 gaagaagagg aagtgttcaa gaaggcccg tctactaatt cgggagcaga cgagactggt 720
454 ttgatgtcag ataaagagtt tgatgattct gcatattcac ccgattattt gtttgaagag 780
456 aatttgtgga ataaacaaa tcatccagat acaaatcata aaaccaaaaa atatactgag 840
458 aatgtggttg aaaatctaga ttctccacca aatgatacat ctgcgtacaa ttcaagtttt 900
460 catgatgaaa ctaatattca aaatgagatc caaataccag aaaatgacga gtatgtacca 960
462 cagatgaaag ctacatccag tgtcaataat accaccatcc ctgcacaaag aagacatgag 1020
464 tcaactttcca cttctgaaaa caaaagaagg aaatttgaaa cagccgacgt tgggggttgat 1080
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474 aatgcttcca agaataccga aaacaaactc cactctaatt tcaaagataa agatgaagga 1380
476 ataattgatg ttgaagctta cgtacctgat gtcaaagcag caactcaaaa caccacccca 1440

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478 gcaacaggac aaacatcagc aaggtcggaa aaactgccac ccttacctac tcatattcca 1500
480 aatccatoga ccatgaatga agctcgacct catccaacaa ctccacataa aagatcaaaa 1560
482 gtcattttcg atttaaaaga tttagaacaa aagttaggta atgatattga ggatttgat 1620
484 tttaaggata tgtatgagag tttgcctgac cattcaagta aggcaacacc taaagacgat 1680
486 attttaaccc gttctaaaag aagactttat acatataccg atggaacatc aaaggctgaa 1740
488 acgttatcta caccaatgaa caaaaatect gttcgtggac atagtacca gaaaaagctt 1800
490 agtatgttgg acatgcatgc gtcttctaaa attcaaagtc ttttacctcc acaaccgcca 1860
492 caaatgtcaa ttgaccttc tgtttccaag caagtgtggg ctaaatacgt tgatgcaatc 1920
494 ttgacttatc aaagagaatt tttcaattat aaaaaagtga ttgttcaata ccaaatggaa 1980
496 cggataaaca aagaccttga acattttgac gatataaatg atggttcaca cactgagaat 2040
498 ttggatactt tcaagcattg tttagaacaa gattatttgg ttatgagtga gtttaatgaa 2100
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506 <210> SEQ ID NO: 6

508 <211> LENGTH: 730

510 <212> TYPE: PRT

512 <213> ORGANISM: Candida albicans

516 <400> SEQUENCE: 6

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526 20 25 30
530 Tyr His Pro Asp Lys Thr Pro Arg Arg Glu Asp His Glu Lys Phe Lys
532 35 40 45
536 Glu Ile Asn Ile Ala Tyr Glu Thr Ile Arg Asp Tyr Tyr Gln Glu Asn
538 50 55 60
542 Gly Gln Lys Asn Ser Gln Pro Ile Pro Asn Thr Asn Thr Glu His Asn
544 65 70 75 80
548 Ser His Gln Lys Pro His Tyr Asn Thr Gly Pro Tyr Ser Thr Tyr Arg
550 85 90 95
554 Phe Thr Thr Ser Ser Thr Thr Thr Asp Asn Thr Asn His Thr Gly His
556 100 105 110
560 Ser Ser Ser Arg Phe Thr Tyr Tyr Asn Phe His Gln Lys Ala Gln Glu
562 115 120 125
566 Asn Asn Arg Lys Gln Asp Glu Glu Arg Ala Ala Gln Arg Glu Arg Leu
568 130 135 140
572 Lys Lys Glu Leu Phe Gln Arg Gln Gln Ala Glu Glu Ala Gln Arg Lys
574 145 150 155 160
578 Lys Glu Phe Glu Gln Lys Ala Glu Phe Ile Lys Ala Ser Leu Leu Glu
580 165 170 175
584 Met Arg Arg Arg Glu Ile Glu Arg Arg Lys Gln Gln Lys Glu Arg Glu
586 180 185 190
590 Gln Arg Gln Lys Glu His Glu Ala Lys Arg Asp Ile Arg Ile Gln Gln
592 195 200 205
596 Leu Ser Glu Gln Asp Ser Arg Ser Asn Gln Thr Lys Glu Glu Glu Glu
598 210 215 220
602 Val Phe Lys Lys Ala Arg Ser Thr Asn Ser Gly Ala Asp Glu Thr Gly
604 225 230 235 240
608 Leu Met Ser Asp Lys Glu Phe Asp Asp Ser Ala Tyr Ser Pro Asp Tyr

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Page 5 of 7B

<210> 13

<211> 302

<212> PRT

<213> Candida albicans

<220>

<221> Xaa = any amino acid at positions 58 and 185

**Does Not Comply
Corrected Diskette Needed**

1. Unknowns must be enumerated in fields 221 222 and 223.
2. Field 221 as "variant"
3. Field 222 as location "58 and 185"
4. Field 223 as particular amino proteins

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

VERIFICATION SUMMARY

DATE: 11/14/2001

PATENT APPLICATION: US/09/763,011A

TIME: 13:52:06

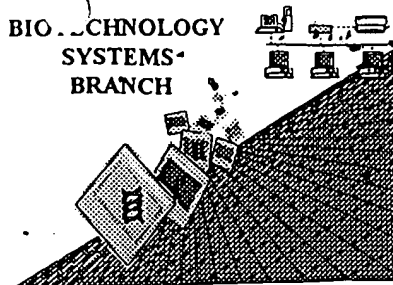
Input Set : A:\JAB-1415.txt

Output Set: N:\CRF3\11142001\I763011A.raw

L:19 M:270 C: Current Application Number differs, Replaced Application Number
L:21 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1041 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
L:1067 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:1067 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13
L:1067 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1115 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
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L:13348 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:114

RAW SEQUENCE LISTING ERROR REPORT

BIO-TECHNOLOGY
SYSTEMS-
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09 763 011A

Source: PCT 09

Date Processed by STIC: 11/14/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>